

IN THE SPECIFICATION

Page 17, amend the paragraph at lines 10-27 as follows:

SEQ ID NO 1 (Fig. 7; GeneBank: accession number AB010697, nucleotides 53939 to 55015; and Stanford University *Arabidopsis thaliana* database: clone number M0J9, gene MOJ9.16 and EST 119G6T7) corresponds to the gene *AtST2a* in *Arabidopsis thaliana*. SEQ ID NO 3 (Fig. 8) is an amino acid sequence deduced from SEQ ID NO 1. This amino acid sequence is of public domain and comes from the Kazusa Arabidopsis Opening Site (KAOS) of the Kazusa DNA Research Institute (KDRI) (~~<http://www.kazusa.or.jp/kaos/>~~; clone number M0J9, gene MOJ9.16). The present inventors have found that the *AtST2a* gene from *Arabidopsis thaliana* encodes a sulfotransferase that sulfonates 12-hydroxyjasmonic acid and 11-hydroxyjasmonic acid with high specificity. Although not shown, results obtained demonstrated that this hydroxyjasmonic acid sulfotransferase exhibits high affinity for its substrate with a K_m value of 11 μM for 12-hydroxyjasmonic acid and 60 μM for 11-hydroxyjasmonic acid. The enzyme did not accept structurally related compounds such as cucurbitic acid, arachidonyl alcohol or prostaglandins. Maximum enzyme activity was observed at pH 7.5 in Tris/HCl buffer and did not require divalent cations for activity. The purified recombinant protein expressed in *E. coli* migrated in SDS-PAGE at a position corresponding to approximately 35,000 daltons (see Fig. 4).

Page 18, amend the paragraph at lines 1-6 as follows:

NO 1. This amino acid sequence is of public domain and comes from the Kazusa Arabidopsis Opening Site (KAOS) of the Kazusa DNA Research Institute (KDRI); (~~<http://www.kazusa.or.jp/kaos/>~~; clone number M0J9, gene MOJ9.15). Amino acid sequence alignment between SEQ ID NOS 3 and 4 indicates that they share 85% amino acid sequence identity and 92% similarity, suggesting that *AtST2a* and *AtST2b* are functional homologues encoding isoenzymes.